

OIPE

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/800,321A

DATE: 01/04/2002
TIME: 15:08:05

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Output Set: N:\CRF3\01042002\I800321A.raw

3 <110> APPLICANT: Padigaru, Muralidhara
4 Burgess, Catherine E
5 Mishra, Vishnu
6 Li, Li
7 Baumgartner, Jason C
8 Majumder, Kumud
9 Spytek, Kimberly A
10 Tchernev, Velizar T
12 <120> TITLE OF INVENTION: Novel Proteins and Nucleic Acids Encoding Same
14 <130> FILE REFERENCE: 15966-703 US
16 <140> CURRENT APPLICATION NUMBER: 09/800,321A
17 <141> CURRENT FILING DATE: 2001-03-05
19 <150> PRIOR APPLICATION NUMBER: 60/186,606
20 <151> PRIOR FILING DATE: 2000-03-03
22 <150> PRIOR APPLICATION NUMBER: 60/221,942
23 <151> PRIOR FILING DATE: 2000-07-31
25 <150> PRIOR APPLICATION NUMBER: 60/260,285
26 <151> PRIOR FILING DATE: 2001-01-08
28 <150> PRIOR APPLICATION NUMBER: 60/220,263
29 <151> PRIOR FILING DATE: 2000-07-24
31 <150> PRIOR APPLICATION NUMBER: 60/257,600
32 <151> PRIOR FILING DATE: 2000-12-21
34 <150> PRIOR APPLICATION NUMBER: 60/187,295
35 <151> PRIOR FILING DATE: 2000-03-06
37 <150> PRIOR APPLICATION NUMBER: 60/219,854
38 <151> PRIOR FILING DATE: 2000-07-21
40 <150> PRIOR APPLICATION NUMBER: 60/187,249
41 <151> PRIOR FILING DATE: 2000-03-06
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56 <151> PRIOR FILING DATE: 2000-03-06
58 <150> PRIOR APPLICATION NUMBER: 60/187,563
59 <151> PRIOR FILING DATE: 2000-03-07
61 <160> NUMBER OF SEQ ID NOS: 78
63 <170> SOFTWARE: PatentIn Ver. 2.1
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66 <211> LENGTH: 993
67 <212> TYPE: DNA
68 <213> ORGANISM: Homo sapiens
70 <400> SEQUENCE: 1

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73 ctgtgaccat ctttggcaat ctgaccatta ttctagtgtc acgcctggac accaaacttc 180
74 ataccccat gtattttttt cttaccaatc tatcactcct ggatctttgt tacaccacat 240
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82 tatcatatgc ttttattgtc cgagcagtat tgaggatata gtctgctgaa ggtcgacaaa 720
83 aagcatttgg gacatgtggt tcccatctaa ttgtggtgtc tcttttttat agtacagccg 780
84 tctctgtgta cctgcaacca ccttcgcccc gctccaagga ccaaggaaag atggtttctc 840
85 tcttctatgg aatcattgca cccatgctga atcccccttat atatacactt aggaacaagg 900
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93 <213> ORGANISM: Homo sapiens

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99 Phe Ser Asp Arg Pro Trp Leu Glu Phe Pro Leu Leu Val Val Phe Leu
100           20           25           30
102 Ile Ser Tyr Thr Val Thr Ile Phe Gly Asn Leu Thr Ile Ile Leu Val
103           35           40           45
105 Ser Arg Leu Asp Thr Lys Leu His Thr Pro Met Tyr Phe Phe Leu Thr
106           50           55           60
108 Asn Leu Ser Leu Leu Asp Leu Cys Tyr Thr Thr Cys Thr Val Pro Gln
109           65           70           75           80
111 Met Leu Val Asn Leu Cys Ser Ile Arg Lys Val Ile Ser Tyr Arg Gly
112           85           90           95
114 Cys Val Ala Gln Leu Phe Ile Phe Leu Ala Leu Gly Ala Thr Glu Tyr
115           100          105          110
117 Leu Leu Leu Ala Val Met Ser Phe Asp Arg Phe Val Ala Ile Cys Arg
118           115          120          125
120 Pro Leu His Tyr Ser Val Ile Met His Gln Arg Leu Cys Leu Gln Leu
121           130          135          140
123 Ala Ala Ala Ser Trp Val Thr Gly Phe Ser Asn Ser Val Trp Leu Ser
124           145          150          155          160
126 Thr Leu Thr Leu Gln Leu Pro Leu Cys Asp Pro Tyr Val Ile Asp His
127           165          170          175
129 Phe Leu Cys Glu Val Pro Ala Leu Leu Lys Leu Ser Cys Val Glu Thr
130           180          185          190
132 Thr Ala Asn Glu Ala Glu Leu Phe Leu Val Ser Glu Leu Phe His Leu
133           195          200          205
135 Ile Pro Leu Thr Leu Ile Leu Ile Ser Tyr Ala Phe Ile Val Arg Ala

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138 Val Leu Arg Ile Gln Ser Ala Glu Gly Arg Gln Lys Ala Phe Gly Thr
139 225      230      235      240
141 Cys Gly Ser His Leu Ile Val Val Ser Leu Phe Tyr Ser Thr Ala Val
142      245      250      255
144 Ser Val Tyr Leu Gln Pro Pro Ser Pro Ser Ser Lys Asp Gln Gly Lys
145      260      265      270
147 Met Val Ser Leu Phe Tyr Gly Ile Ile Ala Pro Met Leu Asn Pro Leu
148      275      280      285
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154 305      310
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158 <211> LENGTH: 943
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164 accttggtcg gagtttccac tccttgtggt ctcttgatt tcttacctg tgaccatctt 120
165 tggcaatctg accattattc tagtgtcacg cctggacacc aaacttcata ccccatgta 180
166 tttttttctt accaatctat cactcctgga tctttgttac accacatgta cagtcccaca 240
167 aatgctagta aatttatgca gcatcaggaa agtaatcagt tatcgtggct gtgtagccca 300
168 gcttttccata tttctggcct tgggggctac tgaatatctt ctctggccg tcatgtcctt 360
169 tgattggttt gtagctatct gtcggcctct ccattactca gttatcatgc accagagact 420
170 ctgcctccag ttggcagctg catcctgggt tactggtttt agtaactcag tgtggttgtc 480
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172 agtccctgca ctgctcaagt tatcttgtgt tgagacaaca gcaaatgagg ctgaactatt 600
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188 1      5      10      15
190 Phe Ser Asp Arg Pro Trp Leu Glu Phe Pro Leu Leu Val Val Phe Leu
191      20      25      30
193 Ile Ser Tyr Thr Val Thr Ile Phe Gly Asn Leu Thr Ile Ile Leu Val
194      35      40      45
196 Ser Arg Leu Asp Thr Lys Leu His Thr Pro Met Tyr Phe Phe Leu Thr
197      50      55      60
199 Asn Leu Ser Leu Leu Asp Leu Cys Tyr Thr Thr Cys Thr Val Pro Gln
200 65      70      75      80

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202 Met Leu Val Asn Leu Cys Ser Ile Arg Lys Val Ile Ser Tyr Arg Gly
203           85           90           95
205 Cys Val Ala Gln Leu Phe Ile Phe Leu Ala Leu Gly Ala Thr Glu Tyr
206           100          105          110
208 Leu Leu Leu Ala Val Met Ser Phe Asp Trp Phe Val Ala Ile Cys Arg
209           115           120           125
211 Pro Leu His Tyr Ser Val Ile Met His Gln Arg Leu Cys Leu Gln Leu
212           130           135           140
214 Ala Ala Ala Ser Trp Val Thr Gly Phe Ser Asn Ser Val Trp Leu Ser
215 145           150           155           160
217 Thr Leu Thr Leu Gln Leu Pro Leu Cys Asp Pro Tyr Val Ile Asp His
218           165           170           175
220 Phe Leu Cys Glu Val Pro Ala Leu Leu Lys Leu Ser Cys Val Glu Thr
221           180           185           190
223 Thr Ala Asn Glu Ala Glu Leu Phe Leu Val Ser Glu Leu Phe His Leu
224           195           200           205
226 Ile Pro Leu Thr Leu Ile Leu Ile Ser Tyr Ala Phe Ile Val Arg Ala
227           210           215           220
229 Val Leu Arg Ile Gln Ser Ala Glu Gly Arg Gln Lys Ala Phe Gly Thr
230 225           230           235           240
232 Cys Gly Ser His Leu Ile Val Val Ser Leu Phe Tyr Ser Thr Ala Val
233           245           250           255
235 Ser Val Tyr Leu Gln Pro Pro Ser Pro Ser Ser Lys Asp Gln Gly Lys
236           260           265           270
238 Met Val Ser Leu Phe Tyr Gly Ile Ile Ala Pro Met Leu Asn Pro Leu
239           275           280           285
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256 atcttttgga atctgacctt tattctagtg tcaagcctgg acaccaaact tcataccccc 180
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259 gccagctttt tcatatttct ggccttgggg gctactgaat atcttctcct ggccgtcatg 360
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261 agactctgcc tccagttggc agctgcatcc tgggttactg gttttagtaa ctcagtgtgg 480
262 ttgtctaccc tgactctcca gctgccactc tgtgaccctt atgtgataga tcactttctc 540
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264 ctattccttg tcagtgagct cttccatcta ataccctga cactcatcct tatatcatat 660
265 gcttttattg tccgagcagt attgaggata cagtctgctg aaggctcgaca aaaagcattt 720
266 gggacatgtg gttcccatct aattgtggtg tctctttttt atagtacagc cgtctctgtg 780
267 taactgcaac caccttcgcc cagctccaag gaccgaggaa agatggtttc tctcttctat 840

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272 <210> SEQ ID NO: 6
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274 <212> TYPE: PRT
275 <213> ORGANISM: Homo sapiens
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282 20 25 30
284 Ile Ser Tyr Thr Val Thr Ile Phe Gly Asn Leu Thr Ile Ile Leu Val
285 35 40 45
287 Ser Arg Leu Asp Thr Lys Leu His Thr Pro Met Tyr Phe Phe Leu Thr
288 50 55 60
290 Asn Leu Ser Leu Leu Asp Leu Cys Tyr Thr Thr Cys Thr Val Pro Gln
291 65 70 75 80
293 Met Leu Val Asn Leu Cys Ser Ile Arg Lys Val Ile Ser Tyr Arg Gly
294 85 90 95
296 Cys Val Ala Gln Leu Phe Ile Phe Leu Ala Leu Gly Ala Thr Glu Tyr
297 100 105 110
299 Leu Leu Leu Ala Val Met Ser Phe Asp Arg Phe Val Ala Ile Cys Arg
300 115 120 125
302 Pro Leu His Tyr Ser Val Ile Met His Gln Arg Leu Cys Leu Gln Leu
303 130 135 140
305 Ala Ala Ala Ser Trp Val Thr Gly Phe Ser Asn Ser Val Trp Leu Ser
306 145 150 155 160
308 Thr Leu Thr Leu Gln Leu Pro Leu Cys Asp Pro Tyr Val Ile Asp His
309 165 170 175
311 Phe Leu Cys Glu Val Pro Ala Leu Leu Lys Leu Ser Cys Val Glu Thr
312 180 185 190
314 Thr Ala Asn Glu Ala Glu Leu Phe Leu Val Ser Glu Leu Phe His Leu
315 195 200 205
317 Ile Pro Leu Thr Leu Ile Leu Ile Ser Tyr Ala Phe Ile Val Arg Ala
318 210 215 220
320 Val Leu Arg Ile Gln Ser Ala Glu Gly Arg Gln Lys Ala Phe Gly Thr
321 225 230 235 240
323 Cys Gly Ser His Leu Ile Val Val Ser Leu Phe Tyr Ser Thr Ala Val
324 245 250 255
326 Ser Val Tyr Leu Gln Pro Pro Ser Pro Ser Ser Lys Asp Arg Gly Lys
327 260 265 270
329 Met Val Ser Leu Phe Tyr Gly Ile Ile Ala Pro Met Leu Asn Pro Leu
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340 <211> LENGTH: 960

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Use of n and/or Xaa has been detected in the Sequence Listing.
 Review the Sequence Listing to insure a corresponding
 explanation is presented in the <220> to <223> fields of
 each sequence using n or Xaa.



VERIFICATION SUMMARY

DATE: 01/04/2002

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Input Set : A:\CURA203U.txt

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L:3209 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:61

L:3648 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:68